Appl. No.: 10/645,863
Response to Office Action dated June 15, 2005

Interview Record Okay
EdT 10/04/2005

SUMMARY OF CLAIMS

Claims 1, 3, 7-10, 14-15, 17-20, 22-27, 29-31, 38 and 41-42 are pending. Claims 2, 16 and 28 are canceled. Claims 4-6, 11-13, 21, 32-37, 39-40 and 43 are withdrawn.

REMARKS

I.   Interview Summary

Applicants wish to thank the Examiner and John Brusca for courtesies extended during a telephonic interview held on August 31, 2005 with Applicants representatives, Vern Norviel and Maya Skubatch, inventor Dr. Jonathan Heller and Dr. Svetlana Shtrom. During the interview, the obviousness rejection in the Final Office Action communicated June 15, 2005 was discussed. Also, the Examiner and Applicants discussed potential ambiguity in step (e). Reconsideration is respectfully requested in light of the following remarks.

II.   Rejections Under 35 U.S.C. §103(a)

Claims 1, 3, 7-10, 14, 15, 17-20, 22-27, 29-31, 38, 41, and 42 were rejected under 35 U.S.C. 103(a) as being unpatentable over Olek et al. in view of Fouillet et al. and with reference to Chambers et al.

Applicants respectfully traverse the above rejection as none of the above references (independently or in combination) teach or suggest all of claimed limitations. For example, none of the above references teach or suggest the limitation of "marketing diagnostic products that use said *representative patterns,*" (Claim 1, emphasis added) wherein the "representative patterns" include 15 markers of unknown specific identity. The term "specific identity" is used throughout the specification and in the claims in its ordinary meaning. A specific identity of a protein would include, for example, amino acid sequence or its function. (See, e.g., Chamber et al. at 283, stating that "protein identification will only be successful if the protein being analysed [*sic*] is represented in the databases. For proteins which have incomplete sequence information, it is necessary to obtain sequence information . . .")

Unlike the claimed invention, the first reference cited by the Examiner, Olek et al. describes "a method for generating a gene panel combining only the advantages of the presently known expression analysis techniques." [Olek et al., Paragraph 61] Such "gene panel" is defined as "a knowledge base, listing, table or other information source, that

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